

84808

STIC-Biotech/Ch mLib

From: Kaushal, Sumesh  
Sent: Tuesday, January 21, 2003 2:15 PM  
To: STIC-Biotech/ChemLib  
Subj ct: 09/734672 SEQ and Interference search

09/734672: SEQ and Interference search

Title: CODING SEQUENCES OF THE HUMAN BRCA1 GENE  
Inventor: MURPHY, PATRICIA

Please search

SEQ ID NO:2  
SEQ ID NO:4

thanks

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CREF

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 1/22  
Date Completed: 1/23  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:

NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

☒ >gi|29725865|gb|AC134684.5| ☐ Homo sapiens chromosome 8, clone RP11-1118M6, complete sequence  
Length = 175202

Score = 32.2 bits (16), Expect = . 14  
Identities = 16/16 (100%)  
Strand = Plus / Minus

Query: 6 acatgacagtgtact 21  
|||||  
Sbjct: 67785 acatgacagtgtact 67770

☒ >gi|24432075|ref|NM\_145268.2| ☐ Homo sapiens LOC136263 (LOC136263), mRNA  
Length = 1953

Score = 32.2 bits (16), Expect = 14  
Identities = 16/16 (100%)  
Strand = Plus / Plus

Query: 6 acatgacagtgtact 21  
|||||  
Sbjct: 459 acatgacagtgtact 474

☐ 1: AC134684

Homo sapiens chromosome 8, clone RP11-1118M6, complete sequence  
gi|29725865|gb|AC134684.5|[29725865]

Links

☐ 2: NM\_145268

Homo sapiens LOC136263 (LOC136263), mRNA  
gi|24432075|ref|NM\_145268.2|[24432075]

Links

Length = 82899

Score = 44.1 bits (22), Expect = 0.004

Identities = 25/26 (96%)

Strand = Plus / Plus

Query: 1      aaaaqacatgacagtqatactttccc 26

|||||

Sbjct: 32876 aaaagacatgacagcgatactttccc 32901

☐ >q1|6552314|ref|NM\_007302.1|

BRCA1-delta9-10, mRNA

Length = 6986

Score = 44.1 bits (22), Expect = 0.004

Identities = 25/26 (96%)

Strand = Plus / Plus

Query: 1      aaaagacatgacagtgatactttccc 26

|||||||

Sbjct: 2086 aaaagacatgacagcgatactttccc 2111

□>qi|6552312|ref|NM\_007301.1|

BRCA1-delta15-17, mRNA

Length = 6519

Score = 44.1 bits (22), Expect = 0.004

Identities = 25/26 (96%)

Strand = Plus / Plus

Query: 1      aaaagacatgacagtgatactttccc 26

|||||

Sbjct: 2209. aaaagacatgacagcgatactttccc 2234

```
>qi|6552310|ref|NM_007300.1|
```

BRCA1-delta14-18, mRNA

Length = 6313

Score = 44.1 bits (22), Expect = 0.004

Identities = 25/26 (96%)

Strand = Plus / Plus

Query: 1      aaaagacatgacagtgatactttccc 26

|||||

Sbjct: 2209 aaaagacatgacagcgatactttccc 2234

BLASTN 2.2.6 [Apr-09-2003]

**Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1055967163-024871-18415

**Query=**

(60 letters)

**Database:** All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)  
1,801,791 sequences; 8,462,007,751 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

**Distribution of 103 Blast Hits on the Query Sequence**

Mouse-over to show define and scores. Click to show alignments

